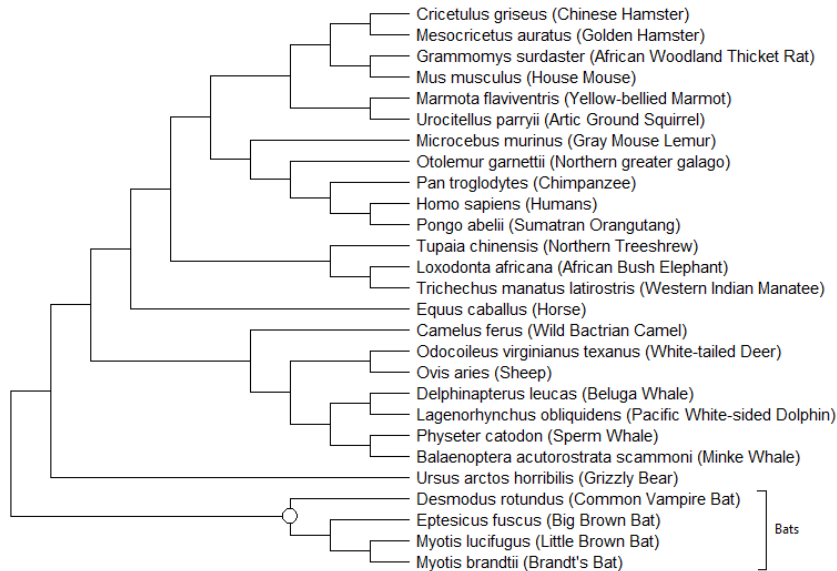
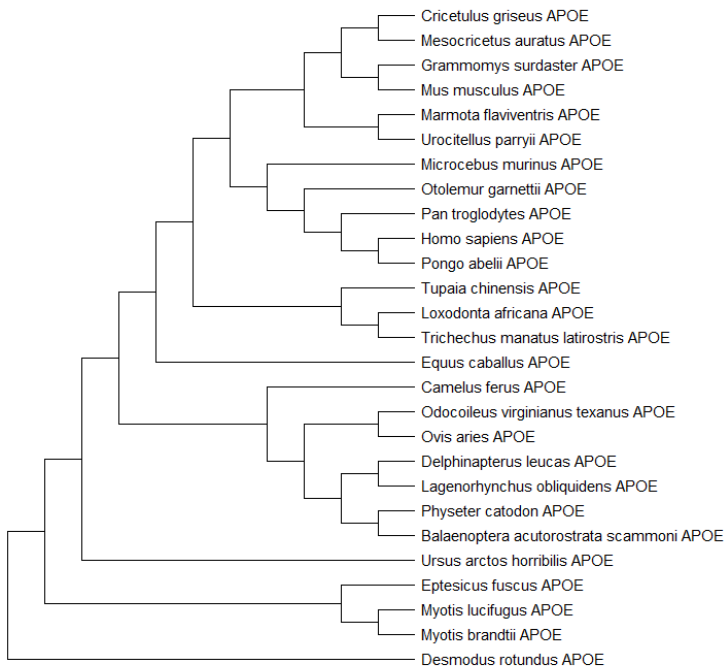


For this week's assignment, I went through the instructions detailed and generated an SPR tree (which I then edited to have the "common" names of my taxa) and a TBR tree. My SPR and TBR tree look completely identical. In both, only 1 parsimony tree was generated.

SPR:



TBR:



Below, I have included the settings I used for both my SPR tree and my TBR tree.

Settings for SPR and TBR:

MX: Analysis Preferences

Phylogeny Reconstruction

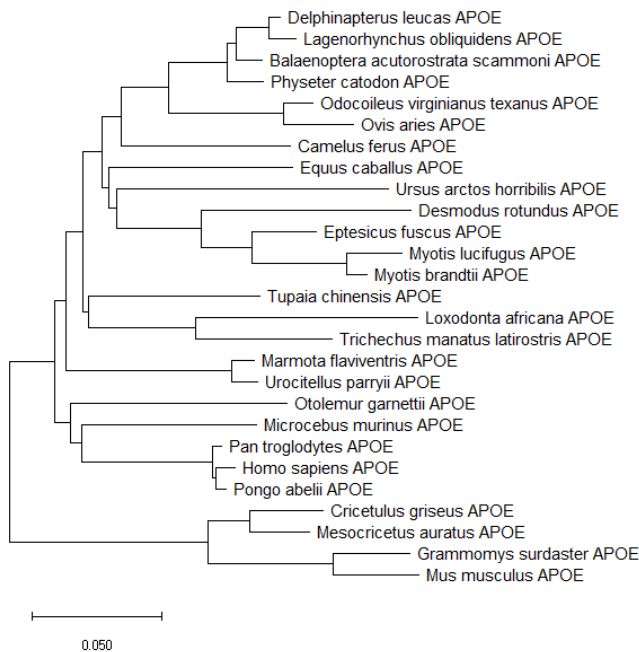
Option	Setting
ANALYSIS	
Statistical Method →	Maximum Parsimony
PHYLOGENY TEST	
Test of Phylogeny →	None
No. of Bootstrap Replications →	Not Applicable
SUBSTITUTION MODEL	
Substitutions Type →	Nucleotide
Genetic Code Table →	Not Applicable
DATA SUBSET TO USE	
Gaps/Missing Data Treatment →	Complete deletion
Site Coverage Cutoff (%) →	Not Applicable
Select Codon Positions →	<input checked="" type="checkbox"/> 1st <input checked="" type="checkbox"/> 2nd <input checked="" type="checkbox"/> 3rd <input checked="" type="checkbox"/> Noncoding Sites
TREE INFERENCE OPTIONS	
MP Search Method →	Subtree-Pruning-Regrafting (SPR)
No. of Initial Trees (random addition) →	10
MP Search level →	1
Max No. of Trees to Retain →	100
SYSTEM RESOURCE USAGE	
Number of Threads →	Not Applicable

Help

Cancel

OK

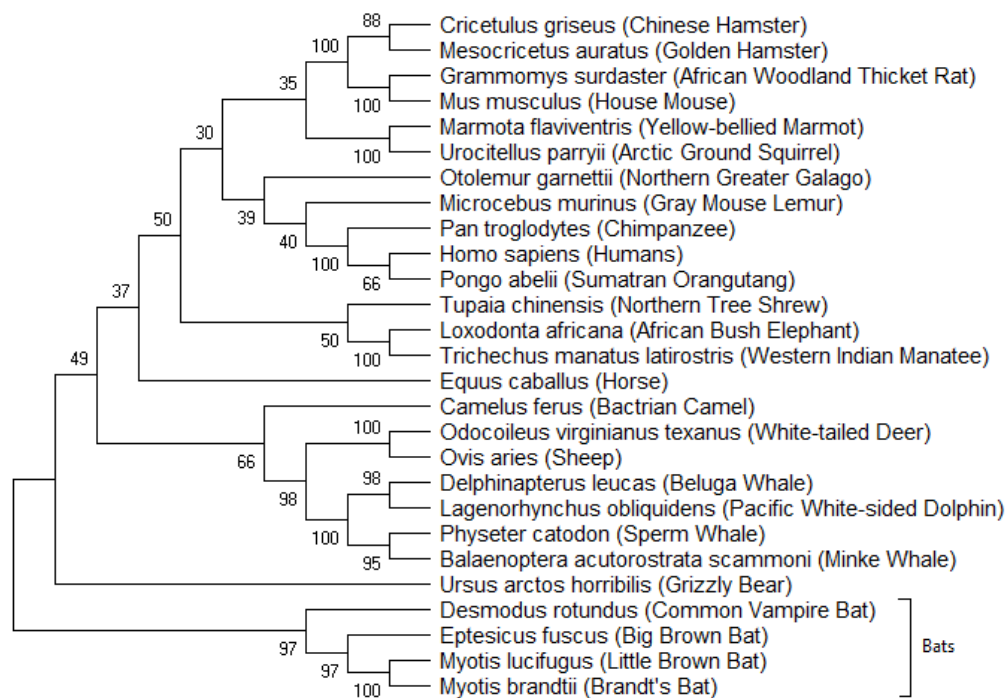
NJ Tree:



My NJ tree compared to my SPR and TBR trees looks slightly different in the ordering. It seems to have put my outgroup as the small mammal group that includes the house mouse, and as we did not learn how to root our trees last week, I did not root my tree using the bat species that I did in my SPR and TBR trees. It appears that most of my closer related species are grouped together similarly between my SPR/TBR trees and my NJ tree, but just the ordering has changed.

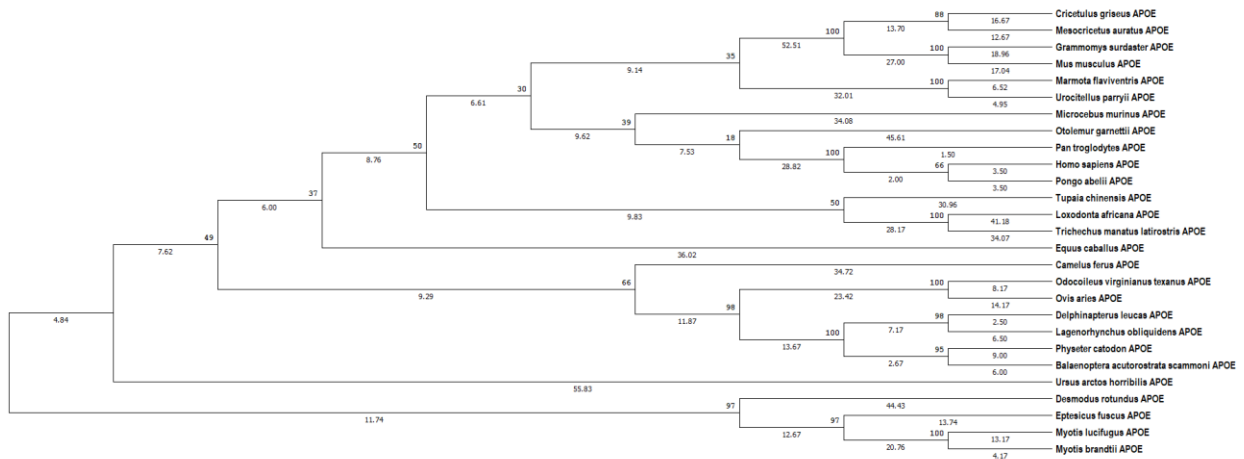
MP Bootstrap Consensus Tree:

My MP Bootstrap tree said there was only 1 parsimony tree that was generated and I set it to 1000 replicates. This tree includes the Bootstrap %, the common names of each taxa, and the subtree of bats, which were my selected outgroup.

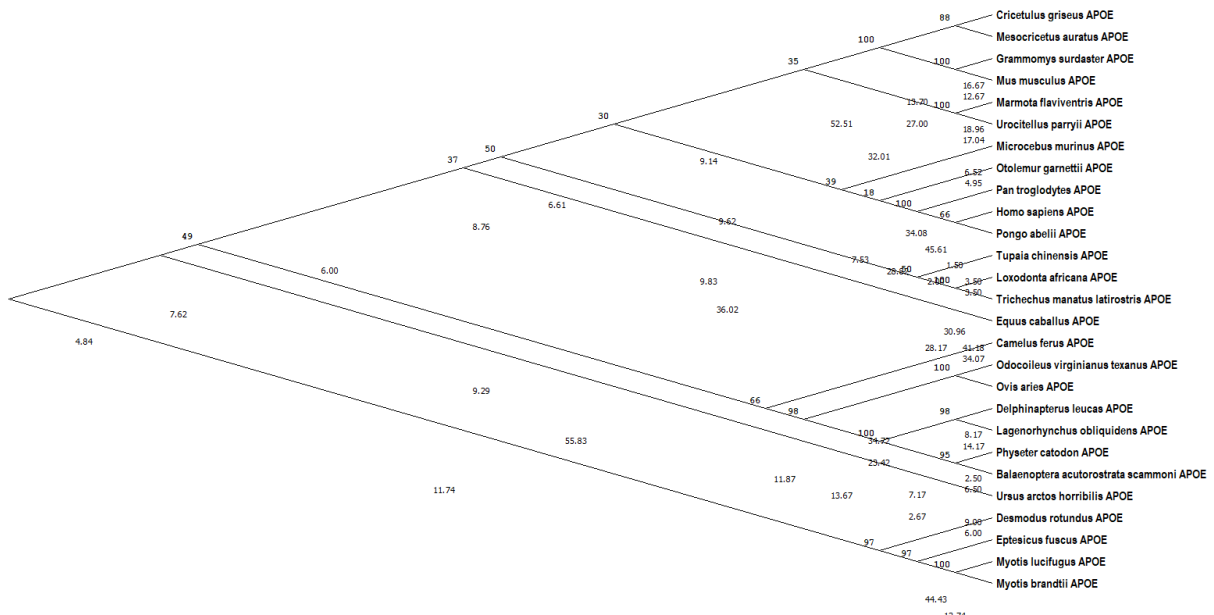


For my three different views of my parsimony tree:

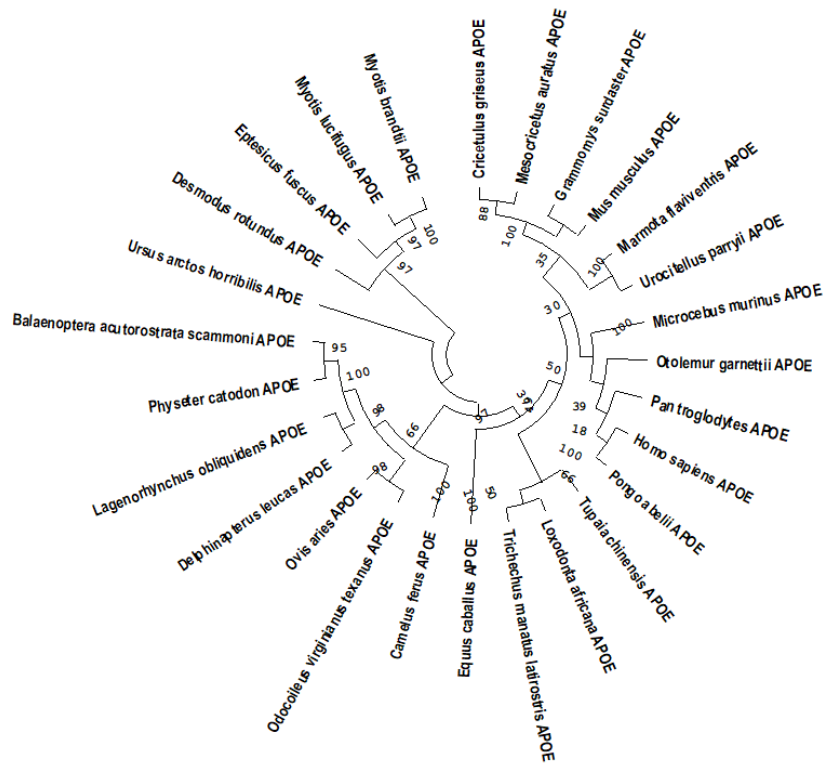
Rectangular:



Straight:



Circular:



The trees that I am constructing are all going towards my goal of determining what new possible animal models could be considered for APOE research to further our understanding of Alzheimer's disease. The tree that I think would be the best visualization of my data and would help in understanding my questions is the rectangular format of my Parsimony tree. In my opinion, the rectangular tree format is clear and concise, with little cluttering of branch length numbers and bootstrap % numbers. The issues that I have with the straight tree is that the options that MEGA gives is pretty limiting on where you can place your numbers and because of the design of the tree, it often messes them up, as seen in my current straight tree. The circular tree is nice, however, in my particular case in trying to find a taxa that might be useful in APOE studies, the relationships between humans and other species is not all that clear.

I think some things that I could improve on in the future are selecting my species a little more carefully and fully looking into what species my sequences are coming from as well as choosing maybe a more distant outgroup than bat species. As it stands, I selected sequences from species purely in regards to the % coverage found from my BLAST result, thus selecting using statistics and not thinking of them from a biological standpoint. Additionally, my outgroup might be more divergent from the rest of my species, could probably be further divergent such as a bird. I think with this understanding, my next trees will be able to incorporate a more "big picture" understanding of making phylogenetic trees as opposed to just following protocols step by step.

The tree that best tells my story is the rectangular tree, as it is very readable and is very clear on which species are “most closely related” to homo sapiens in regards to APOE and could be good potential targets for APOE studies in the future.